



Fig. S1: Maximum Likelihood phylogenetic tree including multiple outgroup species. Maximum likelihood phylogenetic tree including the study strains of the genus *Asaia* and 12 strains of four genera belonging to the Acetobacteraceae family. The phylogenetic analysis has been performed on a concatenate of 356 core genes. These core genes were selected as follows: present in single copy in all the genomes and without frame shifts or stop codons in the alignment. Bootstrap supporting values are reported on the tree branches.